

FIGURE 1

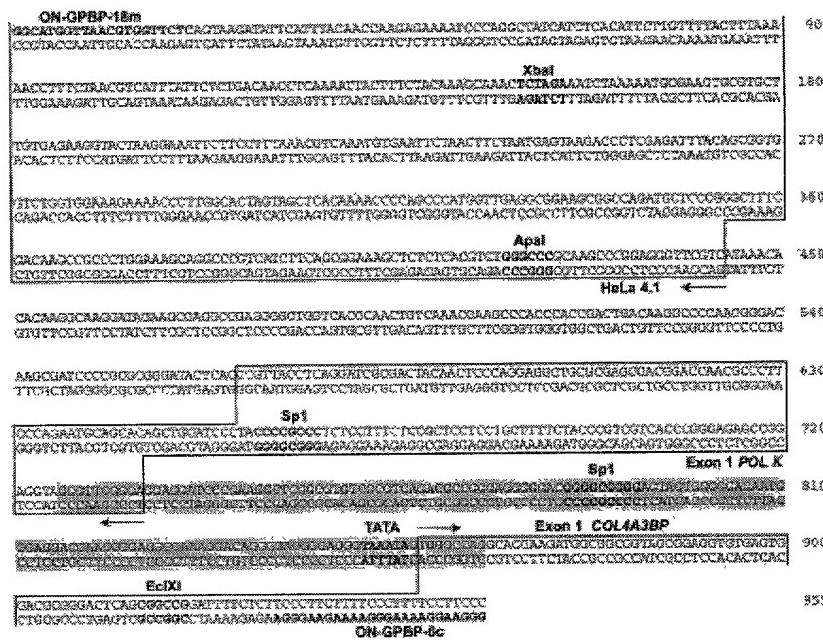
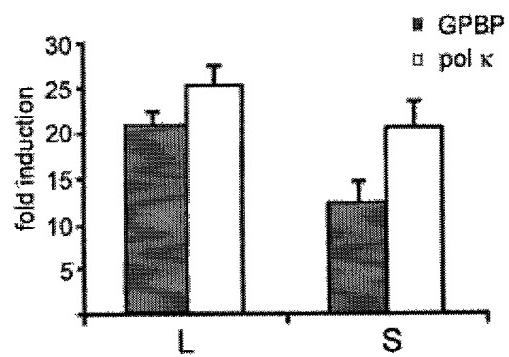


FIGURE 2

A



B

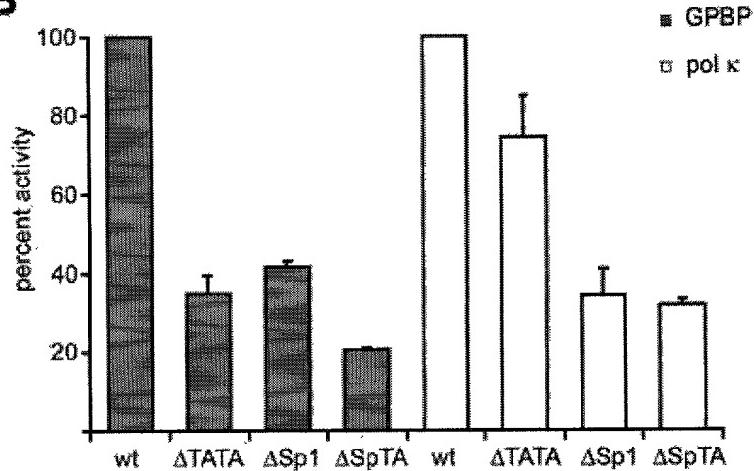
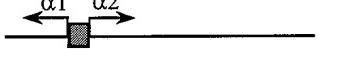
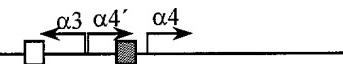
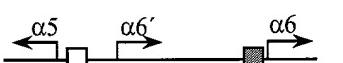


FIGURE 3

	<i>COL4A3BP</i> ■	<i>POLK</i> □	Alignment map*
<i>COL4A1-A2</i> ($\alpha_1\alpha_2$) GenBank no M36963	Region aligned 469-608 $Q=620; E(Q)=591.4\pm17.1$ $z=1.6725, P=\mathbf{0.00472}$	Region aligned 583-722 $Q=580; E(Q)=571\pm19$ $z=0.4737, P=0.3179$	
<i>COL4A3-A4</i> ($\alpha_3\alpha_4$) GenBank no. AF218541	Region aligned 849-990 $Q=674; E(Q)=568.7\pm17.5$ $z=6.0171, P<\mathbf{0.0001}$	Region aligned 182-318 $Q=641; E(Q)=557.5\pm18.4$ $z=4.5380, P<\mathbf{0.0001}$	
<i>COL4A5-A6</i> ($\alpha_5\alpha_6$) GenBank no D28116	Region aligned 1714-1853 $Q=570; E(Q)=524.2\pm18.4$ $z=2.4891, P=\mathbf{0.0064}$	Region aligned 440-579 $Q=570; E(Q)=527.4\pm17.3$ $z=2.4624, P=\mathbf{0.0069}$	

Q is a measure of the quality of the alignment.

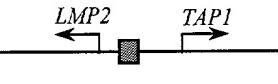
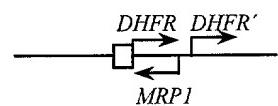
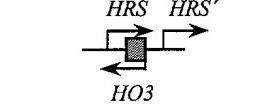
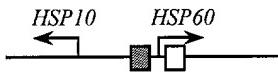
$E(Q)$ is the Q value expected by chance.

z -score for Q . This score is normally distributed with mean zero and variance 1.

P is the probability of observing Q just by chance.

*In the drawing (—→ ~ 0.5 kb) are indicated the statistically significant alignments (P values in ***boldface***).

FIGURE 4

	<i>COL4A3BP</i> ■	<i>POLK</i> □	Alignment map*
<i>LMP2-TAPI</i>	Region aligned 24579-24718 <i>Q</i> =610; <i>E(Q)</i> =549.9±16.9 <i>z</i> =3.5562, <i>P=0.0002</i>	Region aligned 27355-27494 <i>Q</i> =620; <i>E(Q)</i> =582.8±18.6 <i>z</i> =2, <i>P</i> =0.0228	
GenBank no. X66401			
<i>MRP1-DHFR</i>	Region aligned 849-991 <i>Q</i> =581; <i>E(Q)</i> =557.7±20.8 <i>z</i> =1.1202, <i>P</i> =0.1313	Region aligned 704-843 <i>Q</i> =640; <i>E(Q)</i> =553.4±18.1 <i>z</i> =4.7845, <i>P<0.0001</i>	
GenBank no. K01612			
<i>GPAT-AIRC</i>	Region aligned 632-769 <i>Q</i> =554; <i>E(Q)</i> =573.4±20.4 <i>z</i> =-0.9510, <i>P</i> =0.8292	Region aligned 561-705 <i>Q</i> =565; <i>E(Q)</i> =549.4±18.4 <i>z</i> =0.8478, <i>P</i> =0.1983	
GenBank no. U00239			
<i>HO3-HRS</i>	Region aligned 313-452 <i>Q</i> =600; <i>E(Q)</i> =531±17.5 <i>z</i> =3.9429, <i>P<0.0001</i>	Region aligned 214-353 <i>Q</i> =560; <i>E(Q)</i> =557.1±16.2 <i>z</i> =0.1790, <i>P</i> =0.4290	
GenBank no. M96646			
<i>HSP10-HSP60</i>	Region aligned 3451-3590 <i>Q</i> =600; <i>E(Q)</i> =546.7±16.7 <i>z</i> =3.1916, <i>P=0.0007</i>	Region aligned 3684-3821 <i>Q</i> =594; <i>E(Q)</i> =542.6±17.1 <i>z</i> =3.0058, <i>P=0.0013</i>	
GenBank no. AJ250915			
<i>IDHG-TRAPD</i>	Region aligned 16283-16422 <i>Q</i> =622; <i>E(Q)</i> =594.8±16.5 <i>z</i> =2.7394, <i>P</i> =0.0031	Region aligned 14190-14329 <i>Q</i> =610; <i>E(Q)</i> =601.9±15.5 <i>z</i> =0.5226, <i>P</i> =0.3006	
GenBank no. Z68129			

Q is a measure of the quality of the alignment.

E(Q) is the *Q* value expected by chance.

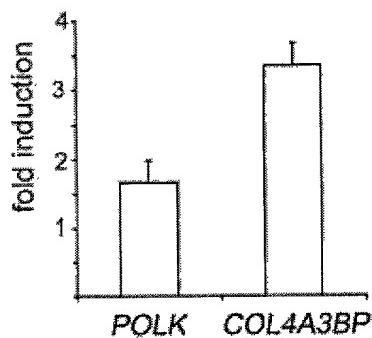
z-score for *Q*. This score is normally distributed with mean zero and variance 1.

P is the probability of observing *Q* just by chance.

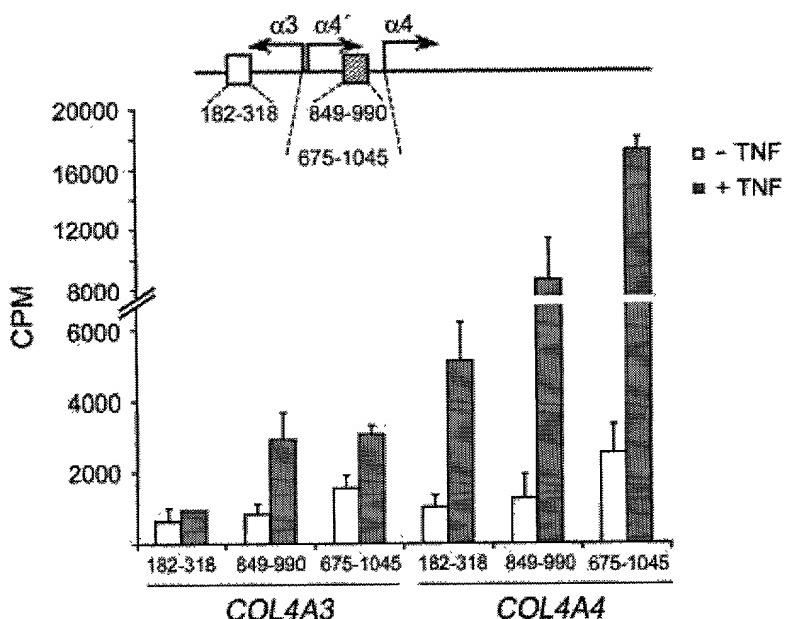
*In the drawing (—~0.5 kb) are indicated the significant alignments (*P* values in ***boldface***).

FIGURE 5

A



B



C

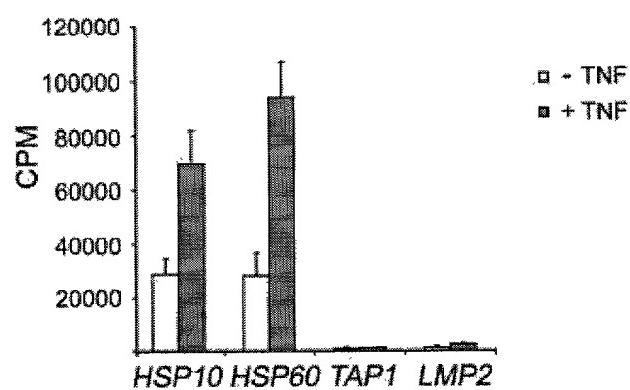


FIGURE 6

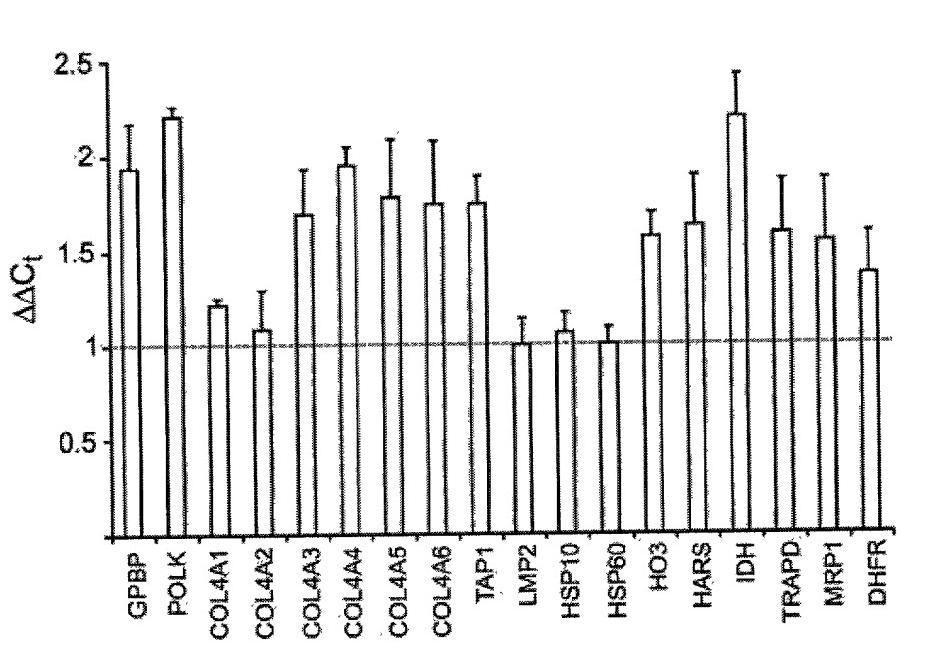


FIGURE 7

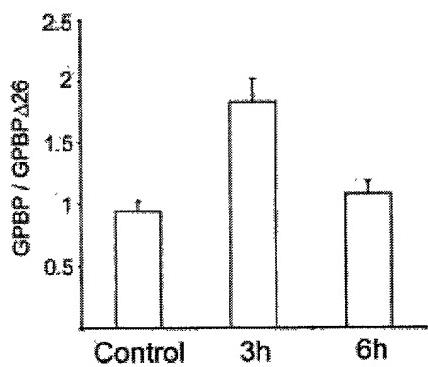
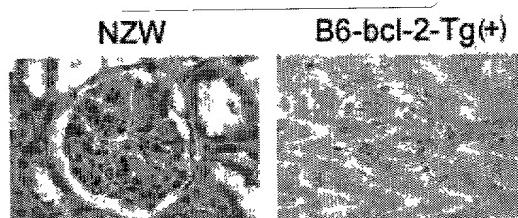


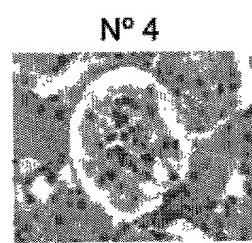
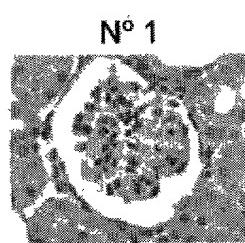
FIGURE 8

A

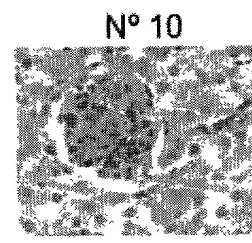
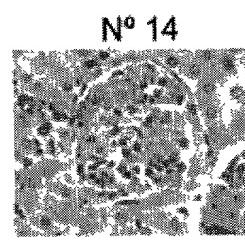


GN:	-	-
GPBP / GPBP Δ 26:	1.6 - 3.0	0.6 - 0.9

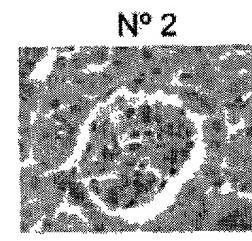
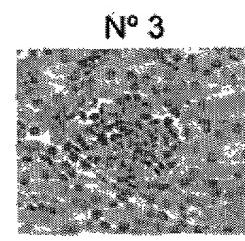
B



GN:	-	-
GPBP / GPBP Δ 26:	2.3	1.9



GN:	+	+
GPBP / GPBP Δ 26:	4.7	4.2



GN:	++	-
GPBP / GPBP Δ 26:	2.5	2.3

α CD4

α CD4 / \emptyset

α CD4 / α TNF

C

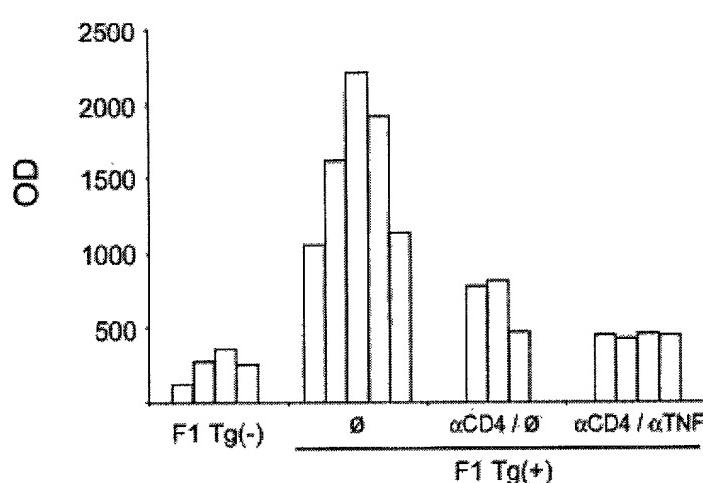


FIGURE 9

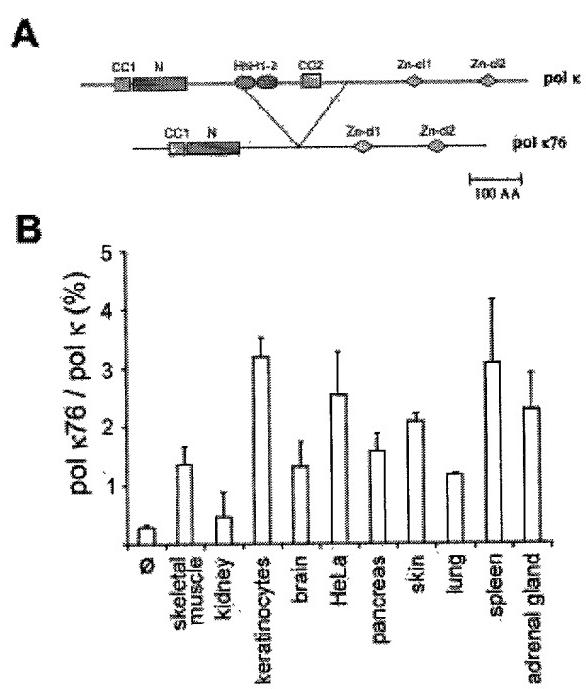


FIGURE 10

